

Appendix II

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with SEQ ID NO: 27
(plasmid pMG) of Perkins et al

>lc1|61939 sid_27
Length=5627

Sort alignments for thi
E value Score Percent
Query start position

Score = 765 bits (414), Expect = 0.0
Identities = 414/414 (100%), Gaps = 0/414 (0%)
Strand=Plus/Plus

Query	770	GCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCCACCCCTTGGCTTCTTAT	829
Sbjct	1879	GCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCCACCCCTTGGCTTCTTAT	1938
Query	830	GCATGCTATACTGTTTTTGGCTTGGGGTCTATACACCCCGCTTCCTCATGTTATAGGTG	889
Sbjct	1939	GCATGCTATACTGTTTTTGGCTTGGGGTCTATACACCCCGCTTCCTCATGTTATAGGTG	1998
Query	890	ATGGTATAGCTTAGCCTATAGGTGTGGGTATTGACCATTATTGACCACTCCCTTATTGG	949
Sbjct	1999	ATGGTATAGCTTAGCCTATAGGTGTGGGTATTGACCATTATTGACCACTCCCTTATTGG	2058
Query	950	TGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACCTCTCTTATTGG	1009
Sbjct	2059	TGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACCTCTCTTATTGG	2118
Query	1010	CTATATGCCAATACACTGTCCTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGG	1069
Sbjct	2119	CTATATGCCAATACACTGTCCTTCAGAGACTGACACGGACTCTGTATTTTACAGGATGG	2178
Query	1070	GGTCTCATTTATTATTATTTACAAATTCACATATACAACACCACCGTCCCCAGTGCCCGCAGT	1129
Sbjct	2179	GGTCTCATTTATTATTATTTACAAATTCACATATACAACACCACCGTCCCCAGTGCCCGCAGT	2238
Query	1130	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGA	1183
Sbjct	2239	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGA	2292

Score = 215 bits (116), Expect = 4e-59
Identities = 116/116 (100%), Gaps = 0/116 (0%)
Strand=Plus/Plus

Query	1183	AACGGTGGAGGGCAGTGTAAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAGACA	1242
Sbjct	2607	AACGGTGGAGGGCAGTGTAAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAGACA	2666
Query	1243	TAATAGCTGACAGACTAACAGACTGTTCCCTTCCATGGGTCTTTTCTGCAGTCACC	1298
Sbjct	2667	TAATAGCTGACAGACTAACAGACTGTTCCCTTCCATGGGTCTTTTCTGCAGTCACC	2722